



Unique decision support system for cashew germplasm management

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Abstract

ICAR-Directorate of Cashew Research, Puttur, Karnataka, the lead centre for conducting cashew research in India, conserves the highest number of cashew germplasm accessions in the country in its National Cashew Field Gene Bank. For the first time, a robust decision support system (DSS) has been developed with 478 accessions and 68 characters to manage and better utilise the germplasm resources. In the module, it is possible to select accessions based on multiple character combinations with information such as frequency distribution, images and pie diagrams. This is expected to help all the stakeholders involved in cashew research, production and processing for selection and subsequent utilisation of suitable germplasm accessions. The module can be accessed at <https://cashew.icar.gov.in/dcr/>.

Keywords: Cashew, database, decision support system, germplasm

Introduction

Germplasm conservation and utilisation are the pillars of any crop improvement program. However, in most crops, the aspect of utilisation is rather limited due to non-availability of proper characterisation and evaluation data on germplasm accessions. Sometimes, even when they are available, it is quite difficult to select germplasm accessions having suitable combinations of characters for *per se* or utilisation in breeding programs owing to enormity of quantitative and qualitative data on large number of accessions. In such situations, it is imperative to develop robust database management and retrieval systems. In other words, development of decision support system (DSS) becomes very much necessary. DSS is a total information system management tool (includes database, user-friendly interfaces and selection options) that helps in decision making in an interactive mode by the users. In this case, it is to facilitate selection of suitable cashew germplasm accessions based on the objective.

Data management and retrieval/decision support systems for germplasm resources of numerous crops have been developed by many institutes both at national and international levels. Some noteworthy Indian efforts include, PGR portal developed by ICAR-National Bureau of Plant Genetic Resources, New Delhi, Spicegenes -Spices Germplasm Database by ICAR-Indian Institute of Spices Research (Saji *et al.*, 2012), Coconut, Arecanut and Cocoa germplasm databases developed by ICAR-Central Plantation Crop Research Institute, Kasaragod. At the international level, some initiatives include Genesys, GeneBank project of Japan, GeneBank of International Potato Center, Rice GeneBank collection and information system at IRRI, Philippines, US plant germplasm system, Plant genetic resources system at Wageningen University, Netherlands, Wheat and Maize GeneBank information system at CIMMYT, Mexico and Genetic Resource Unit at World Vegetable Center, Taiwan. However, the cashew germplasm information is not available in any of these national/international

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initiatives except Genesys where information on only four accessions, as of now, is present.

As far as cashew is concerned, a comprehensive dataset on germplasm accessions for 68 characters in excel sheet is being compiled at ICAR-Directorate of Cashew Research, Puttur since 1986 (Nayak *et al.*, 2015) and a database involving 478 accessions in MS-Access was developed for in-house use. A preliminary database, known as 'Cashew Germplasm Selector' with 57 Goan germplasm accessions for seven quantitative characters was developed in MS-Access at ICAR- Central Coastal Agricultural Research Institute, Goa (Desai, 2010). Further, a database of cashew germplasm known as DOCGERM involving 56 accessions was also developed at the Kerala Agricultural University (Jayalekshmy *et al.*, 2008). However, there is a need to develop comprehensive DSS for better management of cashew genetic resources at the Directorate of Cashew Research involving both qualitative and quantitative characters. In view of this, the DSS for cashew has been developed at our centre.

Materials and methods

Database development

The ICAR-Directorate of Cashew Research is the lead agency for cashew research and currently,

it conserves about 539 accessions in its National Cashew Field Gene Bank (NCFGB). The field evaluation and characterization after six annual harvests was done for 478 accessions. Six grafts of these accessions were maintained with a spacing of 6 m x 6 m following "Cashew Descriptors" of the Bioversity International (IBPGR, 1986). The data on these accessions includes a total of 68 characters involving 27 quantitative characters and 41 qualitative characters. RHS colour chart was used for recording the colour of mature cashew apple (Anonymous, 1995). After evaluation, four grafts per accession with spacing of 4m x 4m were maintained in the field gene bank following recommended package of practices. Further, five germplasm catalogues have been published using the data generated on 478 accessions (Nayak *et al.*, 2015).

The DSS for cashew germplasm management has been developed using (<https://cashew.icar.gov.in/dcr/>) the following technology stack. The database on 478 accessions with 68 characters was developed using MySQL. For front end (user interface), HTML5, CSS3, Twitter Bootstrap, jQuery, Masonry-jQuery, Select2-jQuery, amCharts, FlexSlider-jQuery have been deployed. A PHP5 framework-Laravel was used for backend (server side).



Fig. 1. Landing page of decision support system on cashew

The database is open ended and it is possible to add any number of accessions with data, images and characters as and when they are made available through characterisation of germplasm accessions. Further, this system is accessible across different devices and platforms.

Currently the DSS hosts data on 478 accessions with 68 evaluation characters (both vegetative and reproductive) in addition to 10 important fields from passport data. The DSS aims to retrieve accessions at two levels General search and Search as per descriptor.

Access to information

Upon giving username and password, the search box appears and in this interface, it is possible to select one or many combination of characters. Once the cursor is taken to search box, the drop down menu of characters appears and from this the required character can be selected. The option for typing the required character akin to Google instant facility is also set in the search box. Once the character is selected, frequency distribution pattern and percentage of accessions in different categories as per descriptor will be displayed. Frequency distribution graphs will give an idea of skewness

of character and pie diagrams gives an idea of the number of accessions present in different categories for the selected character.

The major difference between ‘General search’ and ‘Search as per descriptor’ is the way in the option for selection is provided for quantitative characters. For instance, if the character selected is ‘Apple to nut ratio’, then in ‘General search’ the range for this character will be displayed (1.97- 28.1) and user can specify the required range and get the accessions. Whereas in ‘Search as per descriptor’, the categories of this character as per descriptor [low (<6.0), Medium (6-12) and High (>12.0)] will be displayed and user can select any one and get the accessions in that category. Images are also provided for each category to facilitate the process of selection. If no categories exist as per descriptor for any quantitative character, then actual values present in the database will be displayed in ‘Search as per descriptor’. Likewise, it is possible to select the range/categories in two or more combinations of characters at a time in both ‘General Search’ and ‘Search as per descriptor’ and then search for the accessions. In the result table also, a ‘search’ facility is given for locating different fields of accessions. Further, here it is possible to retrieve images of different plant

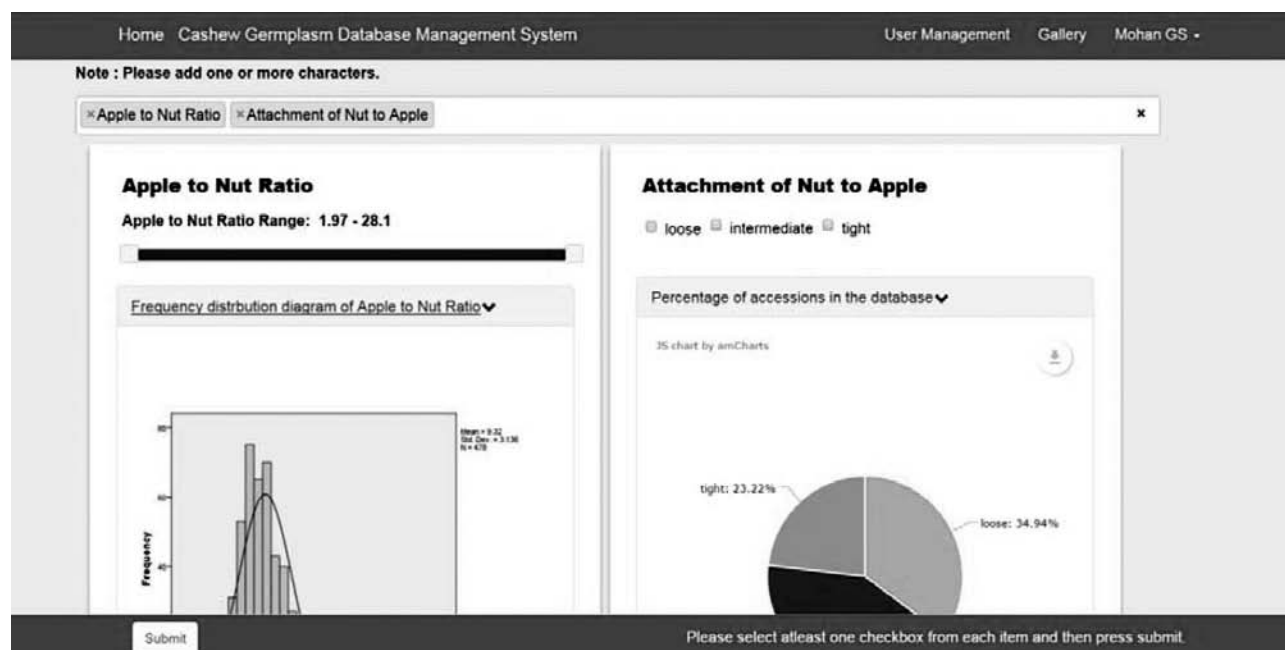


Fig. 2. Search interface in decision support system on cashew

parts for each accession. The resultant data can also be exported to MS-Excel for further use.

Results and discussion

The DSS for cashew germplasm management helps in selection of accessions based on the requirement of the user. For instance, breeder can zero in on the accessions having one or more desirable characters and use them *per se* or in crossing programs. Horticulturists can choose accessions based on agronomic requirements such as tree height, spread, flowering duration *etc.* On the other hand, crop protection workers can select accessions based on characters such as odour of leaves, ease of peeling bark from twigs, cracks on trunk bark *etc.* which might have implications in insect tolerance. It is also feasible to pick accessions

with suitable apple and nut characters for value addition studies. To conduct studies on processing aspects, user can decide accessions based on shelling percentage, kernel weight, apple to nut ratio *etc.*

The frequency distribution patterns provided in the DSS for quantitative characters give an idea of mean, standard deviation, skewness, kurtosis and variability patterns for a particular character. Whereas, pie diagrams for qualitative characters indicate the proportion of accessions for each character. For instance, highly positively skewed distribution was observed for characters such as nut weight, sex ratio, apple weight and apple to nut ratio. This indicates that it is difficult to find accessions with required higher values for these characters in the database. Most quantitative characters except

Table 1. Number of accessions for combination of some traits

a) Colour of mature apple with cumulative yield

Trait		Cumulative yield (kg plant ⁻¹)			Total
Categories		Low (<9)	Medium (9-18)	High (> 18)	
Colour of mature apple	Yellow	134	111	23	268
	Red	64	80	15	159
	Yellow Red	13	28	10	51
	Red Purple	0	0	0	0
	Total	211	219	48	478

b) Tree height (m) with cumulative yield

Trait		Cumulative yield (kg plant ⁻¹)			Total
Categories		Low (<9)	Medium (9-18)	High (> 18)	
Tree height (m)	Dwarf (<2.5)	2	1	0	3
	Semi tall (2.5-4.0)	71	57	4	132
	Tall (> 4.0)	138	161	44	343
	Total	211	219	48	478

c) Nut weight, apple to nut ratio and cumulative yield

Trait		Apple to nut ratio			Cumulative yield (kg plant ⁻¹)
Categories		Low (<6.0)	Medium (6-12)	High (>12.0)	
Nut weight (g)	Low (<5.0)	2	24	11	Low (<9)
		1	20	7	Medium (9-18)
		0	05	1	High (> 18)
	Intermediate (5-7)	12	54	7	Low (<9)
		8	94	20	Medium (9-18)
		0	20	2	High (> 18)
	High (>7.0)	20	73	8	Low (<9)
		7	44	18	Medium (9-18)
		1	19	0	High (> 18)
	Total	51	353	74	Grand Total = 478

tree height, flowering duration and leaf area showed positive kurtosis, which imply that intermediate values are less likely and central and extreme values are more likely for these characters. This sort of information is crucial in deciding the novelty/worth of germplasm accessions during survey and collection and, their subsequent inclusion in GeneBank.

The user can pick accessions based on single or multiple character combinations from the DSS. For instance, the number of accessions for combination of colour of mature apple with cumulative yield, tree height with cumulative yield is given in the Table 1. Table 1a is an example for the combination of qualitative with quantitative trait whereas Table 1b depicts the combination of quantitative with quantitative trait. For character combination involving three characters *viz.*, nut weight, apple to nut ratio and cumulative yield, the number of accessions is given in the Table 1c. In essence, it is possible to easily select accessions having desirable range for both qualitative and quantitative characters and also based on the combinations of characters.

The present DSS on cashew has the following unique features compared to other data retrieval systems developed at national and international levels.

- a) This is the first ever comprehensive DSS on cashew where 68 characters describing each of the 478 germplasm accessions are included. This information is not present in any of the above initiatives.
- b) The DSS deploys a unique and simple interface for selecting any combination of quantitative and qualitative characters. Moreover, the range and frequency distribution of quantitative characters, categories and images of qualitative characters and proportion of accessions in different categories of the selected character are displayed for better decision making process. The images of each accession can be retrieved for easy identification of the accessions selected.

Conclusion

The easy to use interface and search facility with options for selection of multiple combinations of characters in this Decision Support System on

cashew is going to be immensely useful to all cashew stakeholders. This system is all device and platform responsive and any additional characterisation data can be easily appended to the database and visualized via user interface. This module can be profitably emulated in other crops as well where such options are not readily available.

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